

Table S1 miRNAs displaying >2-fold differential expression in osimertinib-resistant cells compared with parental NCI-H1975 and HCC827 cells

miRNA	HCC827OR/P	NCIH1975OR/P
hsa-miR-34c-5p	6.164627931	2.036730946
hsa-miR-1-5p	6.012987013	2.015209125
hsa-miR-431-5p	5.207792208	2.201520913
hsa-miR-23a-3p	4.417734248	2.305806536
hsa-miR-553	4.130111524	2.25
hsa-miR-494-3p	3.86643026	4.968028419
hsa-miR-507	3.405844156	3.565088757
hsa-miR-630	3.370611183	3.781065089
hsa-miR-331-5p	3.213541667	3.335106383
hsa-miR-24-3p	3.02469365	2.381011911
hsa-miR-548al	3.00487013	2.442666667
hsa-miR-381-5p	2.981412639	2.09
hsa-miR-520g-3p	2.981412639	2.786666667
hsa-miR-652-5p	2.890625	2.786666667
hsa-miR-1288-3p	2.890625	2.573333333
hsa-miR-1469	2.75464684	2.89
hsa-miR-490-3p	2.724675325	2.710059172
hsa-miR-483-5p	2.724675325	2.056
hsa-miR-4532	2.709677419	2.18383659
hsa-miR-519b-3p	2.670995671	2.41
hsa-miR-520a-3p	2.402597403	2.253333333

Table S1 (continued)**Table S1** (continued)

miRNA	HCC827OR/P	NCIH1975OR/P
hsa-miR-4485-3p	2.359327217	2.727121464
hsa-miR-761	2.345	2.493730408
hsa-miR-1202	2.333333333	2.442666667
hsa-miR-154-5p	2.270562771	2.086522463
hsa-miR-642a-3p	2.264525994	2.370901639
hsa-miR-1915-3p	2.247074122	3.644444444
hsa-miR-891b	2.24610052	2.004991681
hsa-miR-1249-5p	2.189125296	2.426035503
hsa-miR-2682-5p	2.13864818	2.137472284
hsa-miR-601	2.136363636	2.801452785
hsa-miR-127-3p	2.115839243	2.352549889
hsa-miR-515-3p	2.098	2.290874525
hsa-miR-451a	2.06122449	2.139053254
hsa-miR-2117	2.042553191	2.75095057
hsa-miR-525-3p	2.006493506	5.79
hsa-miR-675-5p	2.003246753	2.174180328
hsa-miR-372-3p	0.494	0.377742947
hsa-miR-31-5p	0.385570274	0.319497025
hsa-miR-205-5p	0.163417569	0.22766323
hsa-miR-141-3p	0.025227482	0.26373365
hsa-miR-200c-3p	0.007198525	0.066098707
miRNA, microRNA.		

Table S2 Pan-cancer mRNA array (NanoString Technologies)

Probe name	Accession no.	Analyte type	Fold-change	P value	Predicted miR-494-3p target (TargetScan)
SFRP4	NM_003014.2	mRNA	-7.68	0.03856117	Yes
HIST1H3G	NM_003534.2	mRNA	-3.09	0.04174855	Yes
ID4	NM_001546.2	mRNA	-2.94	0.00458963	Yes
HIST1H3B	NM_003537.3	mRNA	-2.86	0.00884692	No
ID1	NM_002165.2	mRNA	-2.8	0.027044	No
H3F3A	NM_002107.3	mRNA	-2.65	0.01241234	Yes
HOXA10	NM_018951.3	mRNA	-2.58	0.00676379	Yes
MCM2	NM_004526.2	mRNA	-2.56	0.00524588	No
SOX17	NM_022454.3	mRNA	-2.41	0.03944924	Yes
CCND1	NM_053056.2	mRNA	-2.39	0.00667244	Yes
SMAD9	NM_005905.2	mRNA	-2.25	0.03530474	Yes
PIK3R5	NM_001142633.1	mRNA	-2.19	0.03369235	No
ID2	NM_002166.4	mRNA	-2.18	0.01790669	No
ZIC2	NM_007129.2	mRNA	-2.18	0.02588118	Yes
PBRM1	NM_181042.3	mRNA	-2.12	0.00590484	Yes
COL5A1	NM_000093.3	mRNA	-2.1	0.04878348	No
FASLG	NM_000639.1	mRNA	-2.09	0.03857623	No
BMP7	NM_001719.1	mRNA	-2.06	0.01473878	No
FST	NM_006350.2	mRNA	2	0.02455003	No
ITGB3	NM_000212.2	mRNA	2.41	0.03204901	No
DKK1	NM_012242.2	mRNA	2.67	0.00541677	No
CLCF1	NM_013246.2	mRNA	3.96	0.01814828	No
THBS1	NM_003246.2	mRNA	4.53	0.04309067	No

Values denote expression fold-changes and P values between HCC827 parental cells expressing a miR-494-3p mimic in combination with osimertinib versus cells expressing a scrambled negative control mimic in combination with osimertinib. Negative fold-change means reduced expression in the miR-494-3p mimic setting. Each condition was assayed in biological duplicates.

Table S3 KEGG-pathway analysis of genes suppressed >2-fold in HCC827 parental cells expressing a miR-494-3p mimic in combination with osimertinib versus cells expressing a scrambled negative control mimic in combination with osimertinib

Pathway	Total	Expected	Hits	P value
TGF-beta signaling pathway	92	0.155	5	2.54E-07
Signaling pathways regulating pluripotency of stem cells	139	0.234	4	6.29E-05
Hippo signaling pathway	154	0.259	4	9.38E-05
WNT signaling pathway	158	0.265	3	0.00206
Cell cycle	124	0.208	2	0.0177
PI3K-Akt signaling pathway	354	0.595	3	0.0193
FoxO signaling pathway	132	0.222	2	0.0199
Apelin signaling pathway	137	0.23	2	0.0214
Measles	138	0.232	2	0.0217
Oxytocin signaling pathway	153	0.257	2	0.0263
Hepatitis C	155	0.26	2	0.0269
Kaposi's sarcoma-associated herpesvirus infection	186	0.313	2	0.0377
Transcriptional misregulation in cancer	186	0.313	2	0.0377
Proteoglycans in cancer	201	0.338	2	0.0434

KEGG pathway analysis was computed through the NetworkAnalyst 3.0 software. KEGG, Kyoto encyclopedia of genes and genomes.